

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Alnemri, Emad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomaselli, Kevin
- (ii) TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
NUCLEIC ACIDS ENCODING AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Seed Intellectual Property Law Group
 - (B) STREET: Suite 6300, 701 Fifth Avenue
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 22-SEPT-2003
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Laherty, Carol D.
 - (B) REGISTRATION NUMBER: 51,909
 - (C) REFERENCE/DOCKET NUMBER: 480140.424D1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1700 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 148..1584

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1..1700
 (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| TGAAGTCTCT TCCCAAGCAA ATGGGAGCTT CTTTGACCT TGGAGCACAC AGAGGATTCT | 60 |
| ACTTTCTTTA AAACTTTGTT TTCAGGCAAT TTCCCTGAGA ACCGTTTACT TCCAGAAGAT | 120 |
| TGGTGGAGCT TGATCTGAAG GCTGGCC ATG AAA TCT CAA GGT CAA CAT TGG | 171 |
| Met Lys Ser Gln Gly Gln His Trp | |
| 1 5 | |
| TAT TCC AGT TCA GAT AAA AAC TGT AAA GTG AGC TTT CGT GAG AAG CTT | 219 |
| Tyr Ser Ser Ser Asp Lys Asn Cys Lys Val Ser Phe Arg Glu Lys Leu | |
| 10 15 20 | |
| CTG ATT ATT GAT TCA AAC CTG GGG GTC CAA GAT GTG GAG AAC CTC AAG | 267 |
| Leu Ile Ile Asp Ser Asn Leu Gly Val Gln Asp Val Glu Asn Leu Lys | |
| 25 30 35 40 | |
| TTT CTC TGC ATA GGA TTG GTC CCC AAC AAG AAG CTG GAG AAG TCC AGC | 315 |
| Phe Leu Cys Ile Gly Leu Val Pro Asn Lys Lys Leu Glu Lys Ser Ser | |
| 45 50 55 | |
| TCA GCC TCA GAT GTT TTT GAA CAT CTC TTG GCA GAG GAT CTG CTG AGT | 363 |
| Ser Ala Ser Asp Val Phe Glu His Leu Leu Ala Glu Asp Leu Leu Ser | |
| 60 65 70 | |
| GAG GAA GAC CCT TTC TTC CTG GCA GAA CTC CTC TAT ATC ATA CGG CAG | 411 |
| Glu Glu Asp Pro Phe Phe Leu Ala Glu Leu Leu Tyr Ile Ile Arg Gln | |
| 75 80 85 | |
| AAG AAG CTG CTG CAG CAC CTC AAC TGT ACC AAA GAG GAA GTG GAG CGA | 459 |
| Lys Lys Leu Leu Gln His Leu Asn Cys Thr Lys Glu Glu Val Glu Arg | |
| 90 95 100 | |
| CTG CTG CCC ACC CGA CAA AGG GTT TCT CTG TTT AGA AAC CTG CTC TAC | 507 |
| Leu Leu Pro Thr Arg Gln Arg Val Ser Leu Phe Arg Asn Leu Leu Tyr | |
| 105 110 115 120 | |
| GAA CTG TCA GAA GGC ATT GAC TCA GAG AAC TTA AAG GAC ATG ATC TTC | 555 |
| Glu Leu Ser Glu Gly Ile Asp Ser Glu Asn Leu Lys Asp Met Ile Phe | |
| 125 130 135 | |
| CTT CTG AAA GAC TCG CTT CCC AAA ACT GAA ATG ACC TCC CTA AGT TTC | 603 |
| Leu Leu Lys Asp Ser Leu Pro Lys Thr Glu Met Thr Ser Leu Ser Phe | |
| 140 145 150 | |
| CTG GCA TTT CTA GAG AAA CAA GGT AAA ATA GAT GAA GAT AAT CTG ACA | 651 |
| Leu Ala Phe Leu Glu Lys Gln Gly Lys Ile Asp Glu Asp Asn Leu Thr | |
| 155 160 165 | |

| | |
|---|------|
| TGC CTG GAG GAC CTC TGC AAA ACA GTT GTA CCT AAA CTT TTG AGA AAC Cys Leu Glu Asp Leu Cys Lys Thr Val Val Pro Lys Leu Leu Arg Asn 170 175 180 | 699 |
| ATA GAG AAA TAC AAA AGA GAG AAA GCT ATC CAG ATA GTG ACA CCT CCT Ile Glu Lys Tyr Lys Arg Glu Lys Ala Ile Gln Ile Val Thr Pro Pro 185 190 195 200 | 747 |
| GTA GAC AAG GAA GCC GAG TCG TAT CAA GGA GAG GAA GAA CTA CTT TCC Val Asp Lys Glu Ala Glu Ser Tyr Gln Gly Glu Glu Glu Leu Val Ser 205 210 215 | 795 |
| CAA ACA GAT GTT AAG ACA TTC TTG GAA GCC TTA CCG AGG GCA GCT GTG Gln Thr Asp Val Lys Thr Phe Leu Glu Ala Leu Pro Arg Ala Ala Val 220 225 230 | 843 |
| TAC AGG ATG AAT CGG AAC CAC AGA GGC CTC TGT GTC ATT GTC AAC AAC Tyr Arg Met Asn Arg Asn His Arg Gly Leu Cys Val Ile Val Asn Asn 235 240 245 | 891 |
| CAC AGC TTT ACC TCC CTG AAG GAC AGA CAA GGA ACC CAT AAA GAT GCT His Ser Phe Thr Ser Leu Lys Asp Arg Gln Gly Thr His Lys Asp Ala 250 255 260 | 939 |
| GAG ATC CTG AGT CAT GTG TTC CAG TGG CTT GGG TTC ACA GTG CAT ATA Glu Ile Leu Ser His Val Phe Gln Trp Leu Gly Phe Thr Val His Ile 265 270 275 280 | 987 |
| CAC AAT AAT GTG ACG AAA GTG GAA ATG GAG ATG GTC CTG CAG AAG CAG His Asn Asn Val Thr Lys Val Glu Met Glu Met Val Leu Gln Lys Gln 285 290 295 | 1035 |
| AAG TGC AAT CCA GCC CAT GCC GAC GGG GAC TGC TTC GTG TTC TGT ATT Lys Cys Asn Pro Ala His Ala Asp Gly Asp Cys Phe Val Phe Cys Ile 300 305 310 | 1083 |
| CTG ACC CAT GGG AGA TTT GGA GCT GTC TAC TCT TCG GAT GAG GCC CTC Leu Thr His Gly Arg Phe Gly Ala Val Tyr Ser Ser Asp Glu Ala Leu 315 320 325 | 1131 |
| ATT CCC ATT CGG GAG ATC ATG TCT CAC TTC ACA GCC CTG CAG TGC CCT Ile Pro Ile Arg Glu Ile Met Ser His Phe Thr Ala Leu Gln Cys Pro 330 335 340 | 1179 |
| AGA CTG GCT GAA AAA CCT AAA CTC TTT TTC ATC CAG GCC TGC CAA GGT Arg Leu Ala Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gln Gly 345 350 355 360 | 1227 |
| GAA GAG ATA CAG CCT TCC GTA TCC ATC GAA GCA GAT GCT CTG AAC CCT Glu Glu Ile Gln Pro Ser Val Ser Ile Glu Ala Asp Ala Leu Asn Pro 365 370 375 | 1275 |
| GAG CAG GCA CCC ACT TCC CTG CAG GAC AGT ATT CCT GCC GAG GCT GAC Glu Gln Ala Pro Thr Ser Leu Gln Asp Ser Ile Pro Ala Glu Ala Asp 380 385 390 | 1323 |

| | |
|---|------|
| TTC CTA CTT GGT CTG GCC ACT GTC CCA GGC TAT GTA TCC TTT CGG CAT | 1371 |
| Phe Leu Leu Gly Leu Ala Thr Val Pro Gly Tyr Val Ser Phe Arg His | |
| 395 400 405 | |
| | |
| GTG GAG GAA GGC AGC TGG TAT ATT CAG TCT CTG TGT AAT CAT CTG AAG | 1419 |
| Val Glu Glu Gly Ser Trp Tyr Ile Gln Ser Leu Cys Asn His Leu Lys | |
| 410 415 420 | |
| | |
| AAA TTG GTC CCA AGA CAT GAA GAC ATC TTA TCC ATC CTC ACT GCT GTC | 1467 |
| Lys Leu Val Pro Arg His Glu Asp Ile Leu Ser Ile Leu Thr Ala Val | |
| 425 430 435 440 | |
| | |
| AAC GAT GAT GTG AGT CGA AGA GTG GAC AAA CAG GGA ACA AAG AAA CAG | 1515 |
| Asn Asp Asp Val Ser Arg Arg Val Asp Lys Gln Gly Thr Lys Lys Gln | |
| 445 450 455 | |
| | |
| ATG CCC CAG CCT GCT TTC ACA CTA AGG AAA AAA CTA GTA TTC CCT GTG | 1563 |
| Met Pro Gln Pro Ala Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Val | |
| 460 465 470 | |
| | |
| CCC CTG GAT GCA CTT TCA ATA TAGCAGAGAG TTTTGTGNTGG TTCTTAGACC | 1614 |
| Pro Leu Asp Ala Leu Ser Ile | |
| 475 | |
| | |
| TCAAACGAAT CATTGGNTAT AACCTCCAGC CTCCTGCCCA GCACAGGAAT CGGTGGTCTC | 1674 |
| | |
| CACCTGTCAT TCTAGAAACA GGAAAC | 1700 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Gln | Gly | Gln | His | Trp | Tyr | Ser | Ser | Ser | Asp | Lys | Asn | Cys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Lys | Val | Ser | Phe | Arg | Glu | Lys | Leu | Leu | Ile | Ile | Asp | Ser | Asn | Leu | Glv |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| | | | | | | | | | | | | | | | |
| Val | Gln | Asp | Val | Glu | Asn | Leu | Lys | Phe | Leu | Cys | Ile | Gly | Leu | Val | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| | | | | | | | | | | | | | | | |
| Asn | Lys | Lys | Leu | Glu | Lys | Ser | Ser | Ser | Ala | Ser | Asp | Val | Phe | Glu | His |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| | | | | | | | | | | | | | | | |
| Leu | Leu | Ala | Glu | Asp | Leu | Leu | Ser | Glu | Glu | Asp | Pro | Phe | Phe | Leu | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| | | | | | | | | | | | | | | | |
| Glu | Leu | Leu | Tyr | Ile | Ile | Arg | Gln | Lys | Lys | Leu | Leu | Gln | His | Leu | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |

Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val
 100 105 110
 Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp Ser
 115 120 125
 Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro Lys
 130 135 140
 Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln Gly
 145 150 155 160
 Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys Thr
 165 170 175
 Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys Arg Glu Lys
 180 185 190
 Ala Ile Gln Ile Val Thr Pro Pro Val Asp Lys Glu Ala Glu Ser Tyr
 195 200 205
 Gln Gly Glu Glu Glu Leu Val Ser Gln Thr Asp Val Lys Thr Phe Leu
 210 215 220
 Glu Ala Leu Pro Arg Ala Ala Val Tyr Arg Met Asn Arg Asn His Arg
 225 230 235 240
 Gly Leu Cys Val Ile Val Asn Asn His Ser Phe Thr Ser Leu Lys Asp
 245 250 255
 Arg Gln Gly Thr His Lys Asp Ala Glu Ile Leu Ser His Val Phe Gln
 260 265 270
 Trp Leu Gly Phe Thr Val His Ile His Asn Asn Val Thr Lys Val Glu
 275 280 285
 Met Glu Met Val Leu Gln Lys Gln Lys Cys Asn Pro Ala His Ala Asp
 290 295 300
 Gly Asp Cys Phe Val Phe Cys Ile Leu Thr His Gly Arg Phe Gly Ala
 305 310 315 320
 Val Tyr Ser Ser Asp Glu Ala Leu Ile Pro Ile Arg Glu Ile Met Ser
 325 330 335
 His Phe Thr Ala Leu Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu
 340 345 350
 Phe Phe Ile Gln Ala Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser
 355 360 365
 Ile Glu Ala Asp Ala Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln
 370 375 380
 Asp Ser Ile Pro Ala Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val
 385 390 395 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY: CDS
(B) LOCATION: 257..1744

(A) NAME/KEY: misc feature
(B) LOCATION: 1..1883
(D) OTHER INFORMATION: /note= "Mch5"

| | | | | | | | | | | | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TGAAGGCTGG | TTGTTTCAGAC | TGAGCTTCCT | GCCTGCCTGT | ACCCCGCCAA | CAGCTTCAGA | 60 | | | | | | | | | | |
| AGAAGGTGAC | TGGTGGCTGC | CTGAGGAATA | CCAGTGGGCA | AGAGAATTAG | CATTTCTGGA | 120 | | | | | | | | | | |
| GCATCTGCTG | TCTGAGCAGC | CCCTGGGTGC | GTCCACTTTC | TGGGCACGTG | AGGTTGGGGC | 180 | | | | | | | | | | |
| TTGGCCGCCT | GAGCCCTTGA | GTTGGTCACT | TGAACCTTGG | GAATATTGAG | ATTATATTCT | 240 | | | | | | | | | | |
| CCTGCCTTTT | AAAAAG | ATG | GAC | TTC | AGC | AGA | AAT | CTT | TAT | GAT | ATT | GGG | 289 | | | |
| | | Met | Asp | Phe | Ser | Arg | Asn | Leu | Tyr | Asp | Ile | Gly | | | | |
| | | 1 | | | | 5 | | | | | 10 | | | | | |
| GAA | CAA | CTG | GAC | AGT | GAA | GAT | CTG | GCC | TCC | CTC | AAG | TTC | CTG | AGC | CTG | 337 |
| Glu | Gln | Leu | Asp | Ser | Glu | Asp | Leu | Ala | Ser | Leu | Lys | Phe | Leu | Ser | Leu | |
| | | | 15 | | | | | 20 | | | | | 25 | | | |
| GAC | TAC | ATT | CCG | CAA | AGG | AAG | CAA | GAA | CCC | ATC | AAG | GAT | GCC | TTG | ATG | 385 |
| Asp | Tyr | Ile | Pro | Gln | Arg | Lys | Gln | Glu | Pro | Ile | Lys | Asp | Ala | Leu | Met | |
| | | 30 | | | | | 35 | | | | | 40 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TTA | TTC | CAG | AGA | CTC | CAG | GAA | AAG | AGA | ATG | TTG | GAG | GAA | AGC | AAT | CTG | 433 |
| Leu | Phe | Gln | Arg | Leu | Gln | Glu | Lys | Arg | Met | Leu | Glu | Glu | Ser | Asn | Leu | |
| | 45 | | | | | 50 | | | | | 55 | | | | | |
| TCC | TTC | CTG | AAG | GAG | CTG | CTC | TTC | CGA | ATT | AAT | AGA | CTG | GAT | TTG | CTG | 481 |
| Ser | Phe | Leu | Lys | Glu | Leu | Leu | Phe | Arg | Ile | Asn | Arg | Leu | Asp | Leu | Leu | |
| 60 | | | | | 65 | | | | 70 | | | | | | 75 | |
| ATT | ACC | TAC | CTA | AAC | ACT | AGA | AAG | GAG | GAG | ATG | GAA | AGG | GAA | CTT | CAG | 529 |
| Ile | Thr | Tyr | Leu | Asn | Thr | Arg | Lys | Glu | Glu | Met | Glu | Arg | Glu | Leu | Gln | |
| | | | | 80 | | | | 85 | | | | | | 90 | | |
| ACA | CCA | GGC | AGG | GCT | CAA | ATT | TCT | GCC | TAC | AGG | TTC | CAC | TTC | TGC | CGC | 577 |
| Thr | Pro | Gly | Arg | Ala | Gln | Ile | Ser | Ala | Tyr | Arg | Phe | His | Phe | Cys | Arg | |
| | | | 95 | | | | | 100 | | | | | 105 | | | |
| ATG | AGC | TGG | GCT | GAA | GCA | AAC | AGC | CAG | TGC | CAG | ACA | CAG | TCT | GTA | CCT | 625 |
| Met | Ser | Trp | Ala | Glu | Ala | Asn | Ser | Gln | Cys | Gln | Thr | Gln | Ser | Val | Pro | |
| | | 110 | | | | | 115 | | | | | 120 | | | | |
| TTC | TGG | CGG | AGG | GTC | GAT | CAT | CTA | TTA | ATA | AGG | GTC | ATG | CTC | TAT | CAG | 673 |
| Phe | Trp | Arg | Arg | Val | Asp | His | Leu | Leu | Ile | Arg | Val | Met | Leu | Tyr | Gln | |
| | 125 | | | | | 130 | | | | | 135 | | | | | |
| ATT | TCA | GAA | GAA | GTG | AGC | AGA | TCA | GAA | TTG | AGG | TCT | TTT | AAG | TTT | CTT | 721 |
| Ile | Ser | Glu | Glu | Val | Ser | Arg | Ser | Glu | Leu | Arg | Ser | Phe | Lys | Phe | Leu | |
| 140 | | | | | 145 | | | | | 150 | | | | | 155 | |
| TTG | CAA | GAG | GAA | ATC | TCC | AAA | TGC | AAA | CTG | GAT | GAT | GAC | ATG | AAC | CTG | 769 |
| Leu | Gln | Glu | Glu | Ile | Ser | Lys | Cys | Lys | Leu | Asp | Asp | Asp | Met | Asn | Leu | |
| | | | | 160 | | | | | 165 | | | | | 170 | | |
| CTG | GAT | ATT | TTC | ATA | GAG | ATG | GAG | AAG | AGG | GTC | ATC | CTG | GGA | GAA | GGA | 817 |
| Leu | Asp | Ile | Phe | Ile | Glu | Met | Glu | Lys | Arg | Val | Ile | Leu | Gly | Glu | Gly | |
| | | | 175 | | | | | 180 | | | | | 185 | | | |
| AAG | TTG | GAC | ATC | CTG | AAA | AGA | GTC | TGT | GCC | CAA | ATC | AAC | AAG | AGC | CTG | 865 |
| Lys | Leu | Asp | Ile | Leu | Lys | Arg | Val | Cys | Ala | Gln | Ile | Asn | Lys | Ser | Leu | |
| | | 190 | | | | | 195 | | | | | 200 | | | | |
| CTG | AAG | ATA | ATC | AAC | GAC | TAT | GAA | GAA | TTC | AGC | AAA | GGG | GAG | GAG | TTG | 913 |
| Leu | Lys | Ile | Ile | Asn | Asp | Tyr | Glu | Glu | Phe | Ser | Lys | Gly | Glu | Glu | Leu | |
| | 205 | | | | 210 | | | | | | 215 | | | | | |
| TGT | GGG | GTA | ATG | ACG | ATG | TCG | GAC | TGT | CCA | AGA | GAA | CAG | GAT | AGT | GAA | 961 |
| Cys | Gly | Val | Met | Thr | Met | Ser | Asp | Cys | Pro | Arg | Glu | Gln | Asp | Ser | Glu | |
| 220 | | | | | 225 | | | | | 230 | | | | | 235 | |
| TCA | CAG | ACT | TTG | GAC | AAA | GTT | TAC | CAA | ATG | AAA | AGC | AAG | CCT | CGG | GGA | 1009 |
| Ser | Gln | Thr | Leu | Asp | Lys | Val | Tyr | Gln | Met | Lys | Ser | Lys | Pro | Arg | Gly | |
| | | | | 240 | | | | 245 | | | | | | 250 | | |
| TAC | TGT | CTG | ATC | ATC | AAC | AAT | CAC | AAT | TTT | GCA | AAA | GCA | CGG | GAG | AAA | 1057 |
| Tyr | Cys | Leu | Ile | Ile | Asn | Asn | His | Asn | Phe | Ala | Lys | Ala | Arg | Glu | Lys | |
| | | | 255 | | | | | 260 | | | | | 265 | | | |

| | |
|---|------|
| GTG CCC AAA CTT CAC AGC ATT AGG GAC AGG AAT GGA ACA CAC TTG GAT Val Pro Lys Leu His Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp 270 275 280 | 1105 |
| GCA GGG GCT TTG ACC ACG ACC TTT GAA GAG CTT CAT TTT GAG ATC AAG Ala Gly Ala Leu Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys 285 290 295 | 1153 |
| CCC CAC CAT GAC TGC ACA GTA GAG CAA ATC TAT GAG ATT TTG AAA ATC Pro His His Asp Cys Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile 300 305 310 315 | 1201 |
| TAC CAA CTC ATG GAC CAC AGT AAC ATG GAC TGC TTC ATC TGC TGT ATC Tyr Gln Leu Met Asp His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile 320 325 330 | 1249 |
| CTC TCC CAT GGA GAC AAG GGC ATC ATC TAT GGC ACT GAT GGA CAG GAG Leu Ser His Gly Asp Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu 335 340 345 | 1297 |
| GCC CCC ATC TAT GAG CTG ACA TCT CAG TTC ACT GGT TTG AAG TGC CCT Ala Pro Ile Tyr Glu Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro 350 355 360 | 1345 |
| TCC CTT GCT GGA AAA CCC AAA GTG TTT TTT ATT CAG GCT TGT CAG GGG Ser Leu Ala Gly Lys Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly 365 370 375 | 1393 |
| GAT AAC TAC CAG AAA GGT ATA CCT GTT GAG ACT GAT TCA GAG GAG CAA Asp Asn Tyr Gln Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln 380 385 390 395 | 1441 |
| CCC TAT TTA GAA ATG GAT TTA TCA TCA CCT CAA ACG AGA TAT ATC CCG Pro Tyr Leu Glu Met Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro 400 405 410 | 1489 |
| GAT GAG GCT GAC TTT CTG CTG GGG ATG GCC ACT GTG AAT AAC TGT GTT Asp Glu Ala Asp Phe Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val 415 420 425 | 1537 |
| TCC TAC CGA AAC CCT GCA GAG GGA ACC TGG TAC ATC CAG TCA CTT TGC Ser Tyr Arg Asn Pro Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys 430 435 440 | 1585 |
| CAG AGC CTG AGA GAG CGA TGT CCT CGA GGC GAT GAT ATT CTC ACC ATC Gln Ser Leu Arg Glu Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile 445 450 455 | 1633 |
| CTG ACT GAA GTG AAC TAT GAA GTA AGC AAC AAG GAT GAC AAG AAA AAC Leu Thr Glu Val Asn Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn 460 465 470 475 | 1681 |
| ATG GGG AAA CAG ATG CCT CAG CCT ACT TTC ACA CTA AGA AAA AAA CTT Met Gly Lys Gln Met Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu 480 485 490 | 1729 |
| GTC TTC CCT TCT GAT TGATGGTGCT ATTTTGTTTG TTTTGTTTTG TTTTGTTTTT | 1784 |

Val Phe Pro Ser Asp
495

TTGAGACAGA ATCTCGCTCT GTCGCCCAGG CTGGAGTGCA GTGGCGTGAT CTCGGCTCAC 1844
CGCAAGCTCC GCCTCCCGGG TTCAGGCCAT TCTCCTGCT 1883

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
1 5 10 15
Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
20 25 30
Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
35 40 45
Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
50 55 60
Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr Leu Asn
65 70 75 80
Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr Pro Gly Arg Ala
85 90 95
Gln Ile Ser Ala Tyr Arg Phe His Phe Cys Arg Met Ser Trp Ala Glu
100 105 110
Ala Asn Ser Gln Cys Gln Thr Gln Ser Val Pro Phe Trp Arg Arg Val
115 120 125
Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val
130 135 140
Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile
145 150 155 160
Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile
165 170 175
Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu
180 185 190
Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys Ile Ile Asn
195 200 205

Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu Cys Gly Val Met Thr
 210 215 220
 Met Ser Asp Cys Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp
 225 230 235 240
 Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile
 245 250 255
 Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His
 260 265 270
 Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr
 275 280 285
 Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His His Asp Cys
 290 295 300
 Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp
 305 310 315 320
 His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp
 325 330 335
 Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu
 340 345 350
 Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys
 355 360 365
 Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys
 370 375 380
 Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met
 385 390 395 400
 Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe
 405 410 415
 Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro
 420 425 430
 Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu
 435 440 445
 Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn
 450 455 460
 Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met
 465 470 475 480
 Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp
 485 490 495

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..19
 - (D) OTHER INFORMATION: /note= "t96-pr1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCAGCCTCGG CAGGAATAC

19

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /note= "SK-Zap"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAATTCG GCACGAG

17

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..18
 - (D) OTHER INFORMATION: /note= "Mch5-pr1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACAGAGCGA GATTCTGT

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCACCATCAA TCAGAAGG

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGAGATCA TGTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Gln Gly

1

5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Arg Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Asp Arg Asn Gly Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Ser His Gly Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..9
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Ile Gln Ala Cys Gln Gly Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..5
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Glu Thr Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Val | Ser | Tyr | Arg | Asn | Pro | Ala | Glu | Gly | Thr | Trp | Tyr | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Arg | Gln | Gly | Thr |
| 1 | | | | 5 | |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Thr His Gly Arg Phe

1

5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..9
 - (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Ile Gln Ala Cys Gln Gly Glu Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Glu Ala Asp Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..15
 (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Tyr | Val | Ser | Phe | Arg | His | Val | Glu | Glu | Gly | Ser | Trp | Tyr | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Gly | Val | Arg | Asn | Gly | Thr |
| 1 | | | | 5 | |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Leu | Ser | His | Gly | Glu | Glu |
| 1 | | | | 5 | |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..9
 - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | Gln | Ala | Cys | Arg | Gly | Thr | Glu |
| 1 | | | | 5 | | | | |

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | |
|-----|-----|-----|-----|-----|
| Ile | Gln | Ala | Asp | Ser |
| 1 | | | | 5 |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Pro Glu Arg Arg Gly Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Ser His Gly Glu Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
- ```

Ile Ile Gln Ala Cys Arg Gly Asn Gln
1 5

```
- (2) INFORMATION FOR SEQ ID NO:30:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
- ```

Thr Glu Val Asp Ala
1           5

```
- (2) INFORMATION FOR SEQ ID NO:31:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Tyr Tyr Ser His Arg Glu Thr Val Asn Gly Ser Trp Tyr Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Ser Arg Ser Gly Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Ser His Gly Glu Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..9
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Ile Gln Ala Cys Arg Gly Thr Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..5
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile Glu Thr Asp Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..15
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "CED-3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Pro Thr Arg Asn Gly Thr
 1 5
- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "CED-3"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Ser His Gly Glu Glu
 1 5
- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..9

(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Val Gln Ala Cys Arg Gly Glu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..5
 (D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp Ser Val Asp Gly
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..15
 (D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Tyr Val Ser Trp Arg Asn Ser Ala Arg Gly Ser Trp Phe Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Pro Arg Arg Thr Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Ser His Gly Ile Arg
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..9
 - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ile Ile Gln Ala Cys Arg Gly Asp Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Trp Phe Lys Asp Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Pro Arg Asn Gly Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ser His Gly Ile Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..9
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ile Val Gln Ala Cys Arg Gly Ala Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Trp Val Lys Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Asn Val Ser Trp Arg Asp Ser Thr Met Gly Ser Ile Phe Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide

- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Ala Arg Asn Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Ser His Gly Ile Leu
1 5

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..9
 - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ile Val Gln Ala Cys Arg Gly Glu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | | | | |
|-----|-----|-----|-----|-----|
| Trp | Val | Arg | Asp | Ser |
| 1 | | | | 5 |

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..15
 - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asn | Val | Ser | Trp | Arg | Asp | Arg | Thr | Arg | Gly | Ser | Ile | Phe | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
 - (B) LOCATION: 1..6
 - (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Phe Arg Ser Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ser His Gly Val Glu
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..9
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Ile Gln Ala Cys Arg Gly Asp Glu
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Gln Gln Asp Gly
1 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Thr Ala Ala Met Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTACAGGAT CCACTTCTGC CGCATGAGC

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
ACTCCTCCCC TTTGCTGAAT TCTTAATAGT CGT

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: .
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: /note= "Mch4 A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly Val
1          5          10          15
Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro Asn
20          25          30
Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His Leu
35          40          45
Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala Glu
50          55          60
Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: /note= "Mch5 A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser Glu Asp Leu
1          5          10          15
Ala Ser Leu Lys Phe Leu Ser Leu Asp Thr Ile Pro Gln Arg Lys Gln
20          25          30
Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu Gln Glu Lys
35          40          45
Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu Leu Leu Phe
50          55          60
Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: /note= "Mch4 B"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp
1           5           10           15
Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro
          20           25           30
Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln
          35           40           45
Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys
          50           55           60
Thr Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys
65           70           75

```

- (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: /note= "Mch5 B"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu
1           5           10           15
Val Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu
          20           25           30
Ile Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe

```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

Gly Ser Trp Phe Ile
1 5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

Gly Ser Trp Tyr Ile
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Asp Glu Val Asp

1

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Val Ala Asp
1

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Glu Thr Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ile Gln Ala Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Glu Ala Asp Ala
1 5